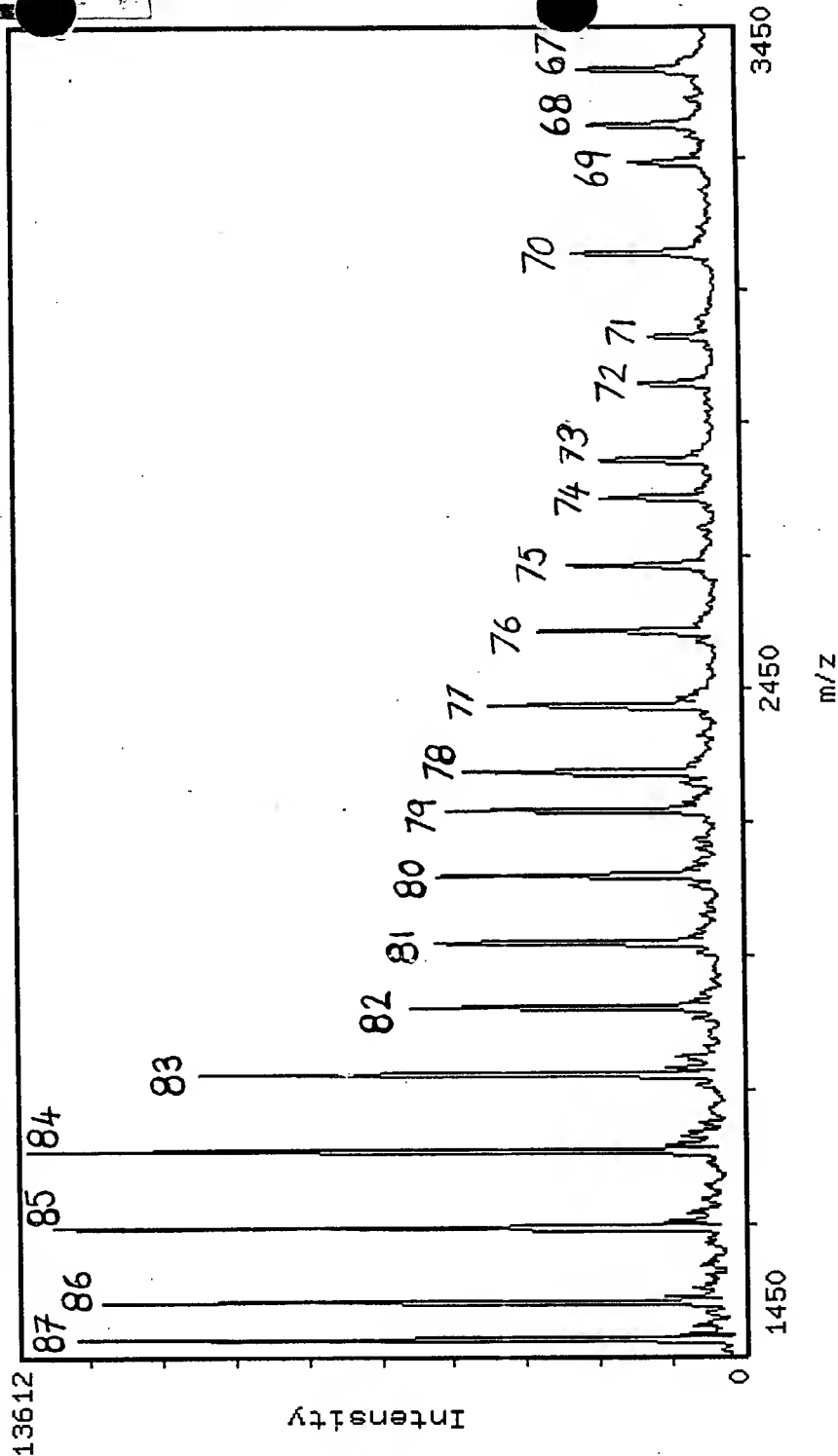


Figure A

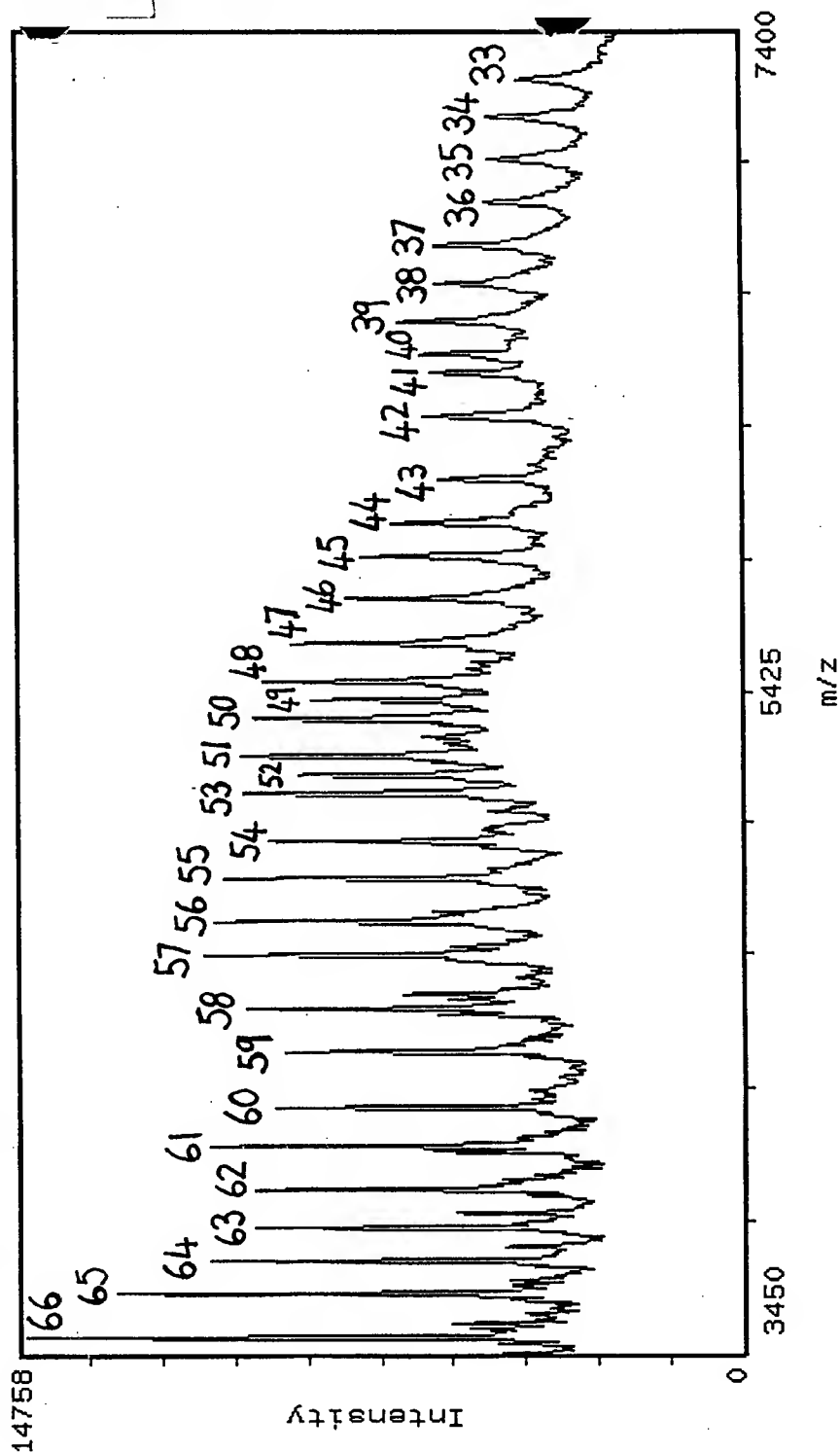
HIV-1 PROTEASE PEPTIDE LADDER (99-N, WHERE N=99,67)



891177

FIGURE B

HIV-1 PROTEASE PEPTIDE LADDER (99-N, WHERE N=66,33)

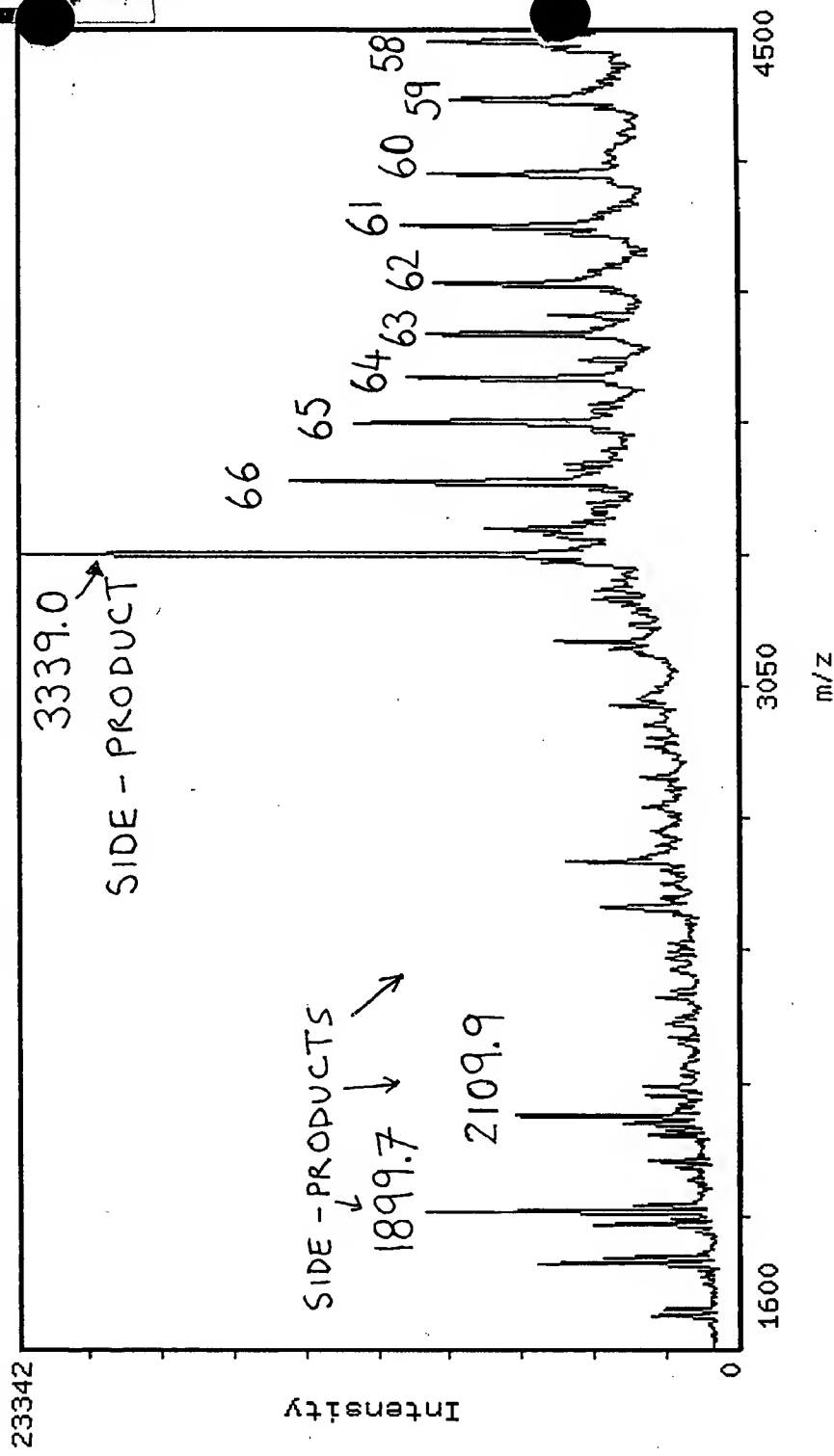


891177

891177

FIGURE C

LOW MASS REGION OF HIV-1 PROTEASE
PEPTIDE LADDER (99-N, WHERE N=66,33)



891177

IDENTIFICATION OF SIDE-REACTION PRODUCT

MEASURED MM OF MAJOR SIDE-PRODUCT = 3339.0

CALCULATED MM OF PEPTIDE (99-69) = 3242.9

DIFFERENCE = 96.1

HIS-69 APPEARS TO BE TRIFLUOROACETYLATED

891177

INTACT STARTING
PEPTIDE CHAIN

1-2-3-4-5-6-7-8-9-.....-n-(OH)

(X)-1-2-3-4-5-6-7-8-9-.....-n-(OH)

(X)-2-3-4-5-6-7-8-9-.....-n-(OH)

(X)-3-4-5-6-7-8-9-.....-n-(OH)

(X)-4-5-6-7-8-9-.....-n-(OH)

(X)-5-6-7-8-9-.....-n-(OH)

(Figure 1)

etc.

891177

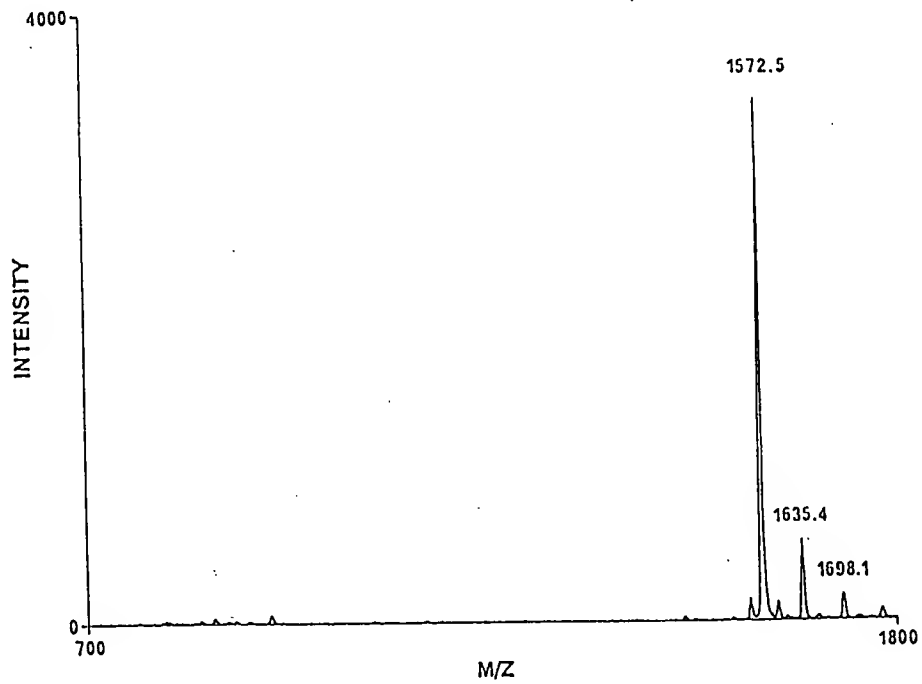


Figure 1.* Positive ion matrix-assisted laser desorption mass spectrum of [Glu¹]-Fibrinopeptide B.

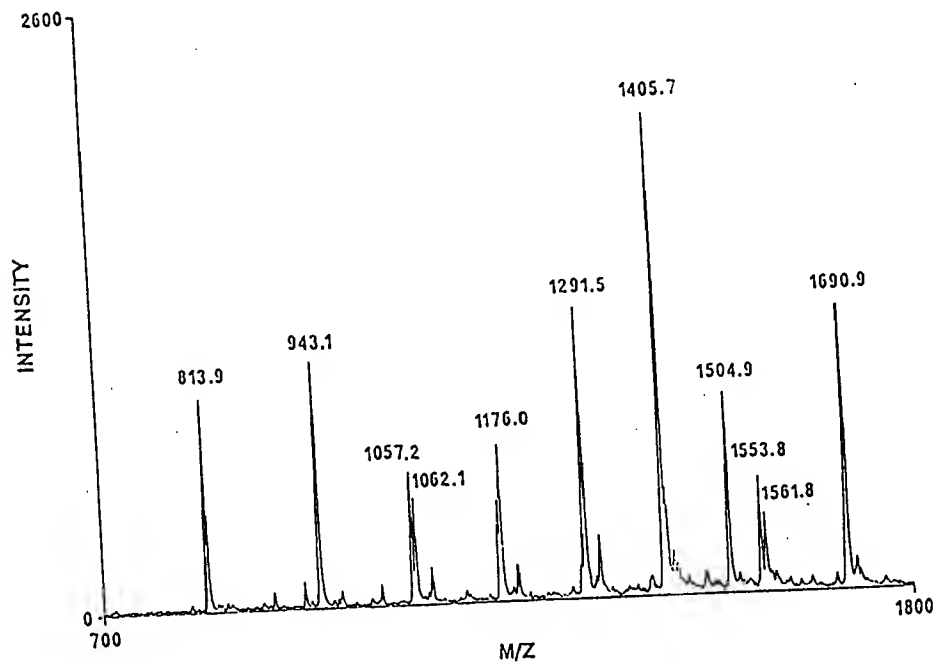
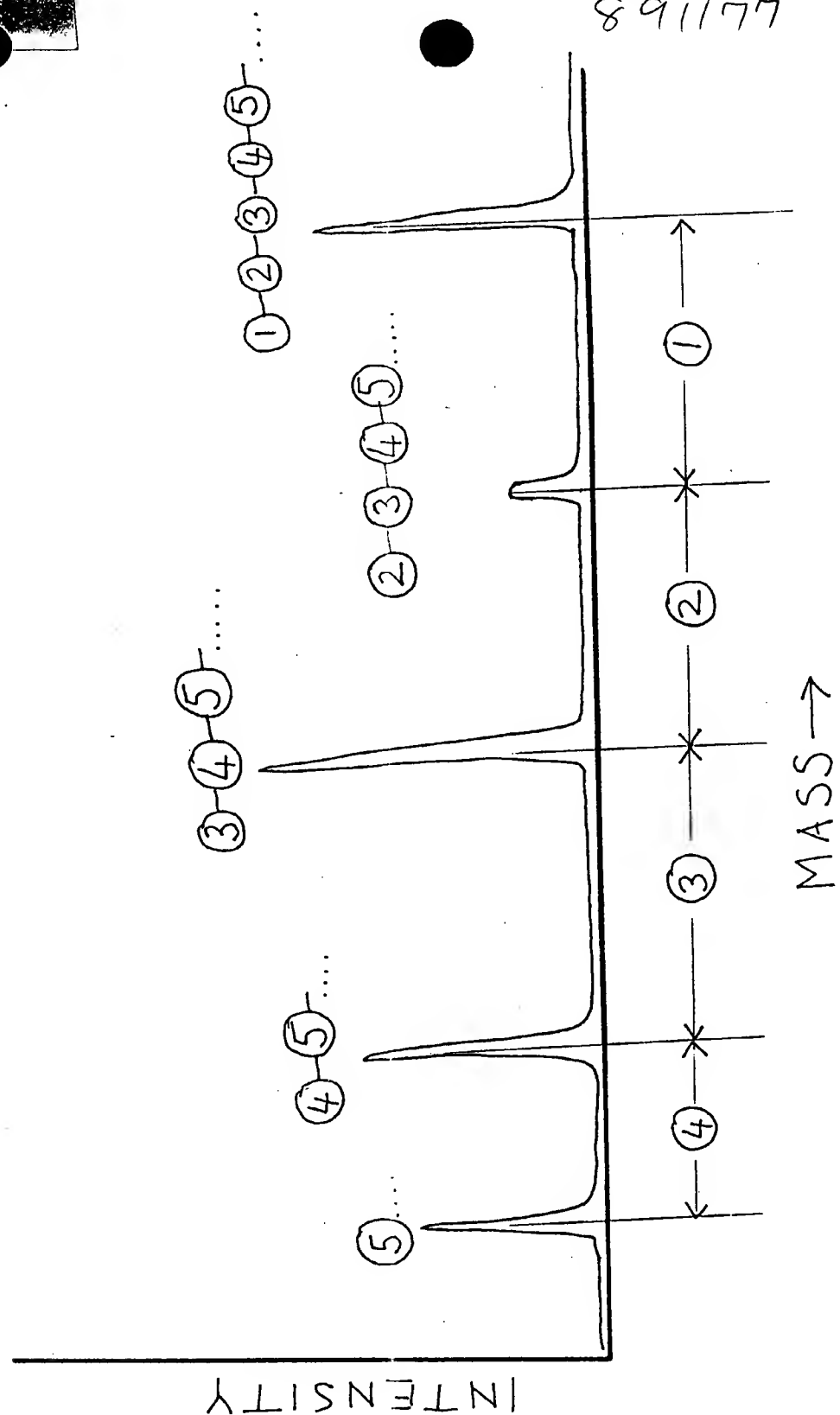
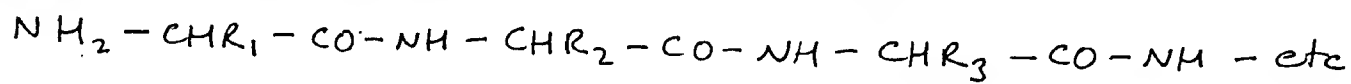
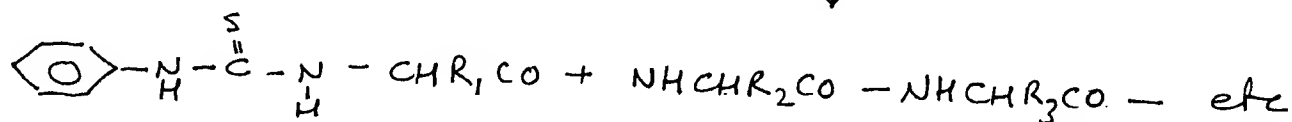
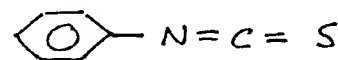
891177
21.

Figure 2.* Positive ion matrix-assisted laser desorption mass spectrum of [Glu¹]-Fibrinopeptide B after 7 cycles of modified Edman degradation.



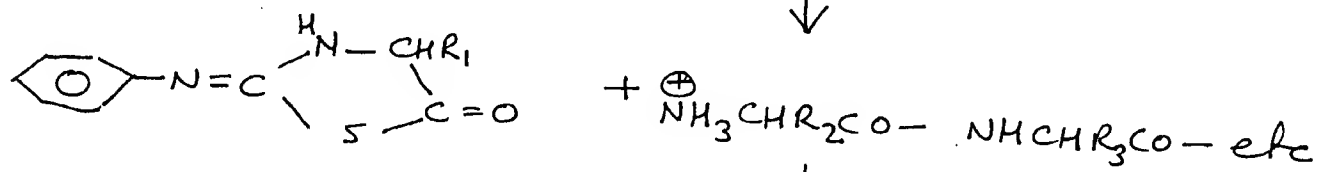


- ① Coupling: PITC in the presence of base.



- ② Wash, dry.

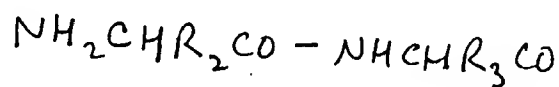
- ③ Cleavage: anhydrous acid



- ④ Wash (removes ATZ/PTH derivative)

- ⑤ Neutralize: base

- ⑥ Wash



Repeat steps 1 — 6

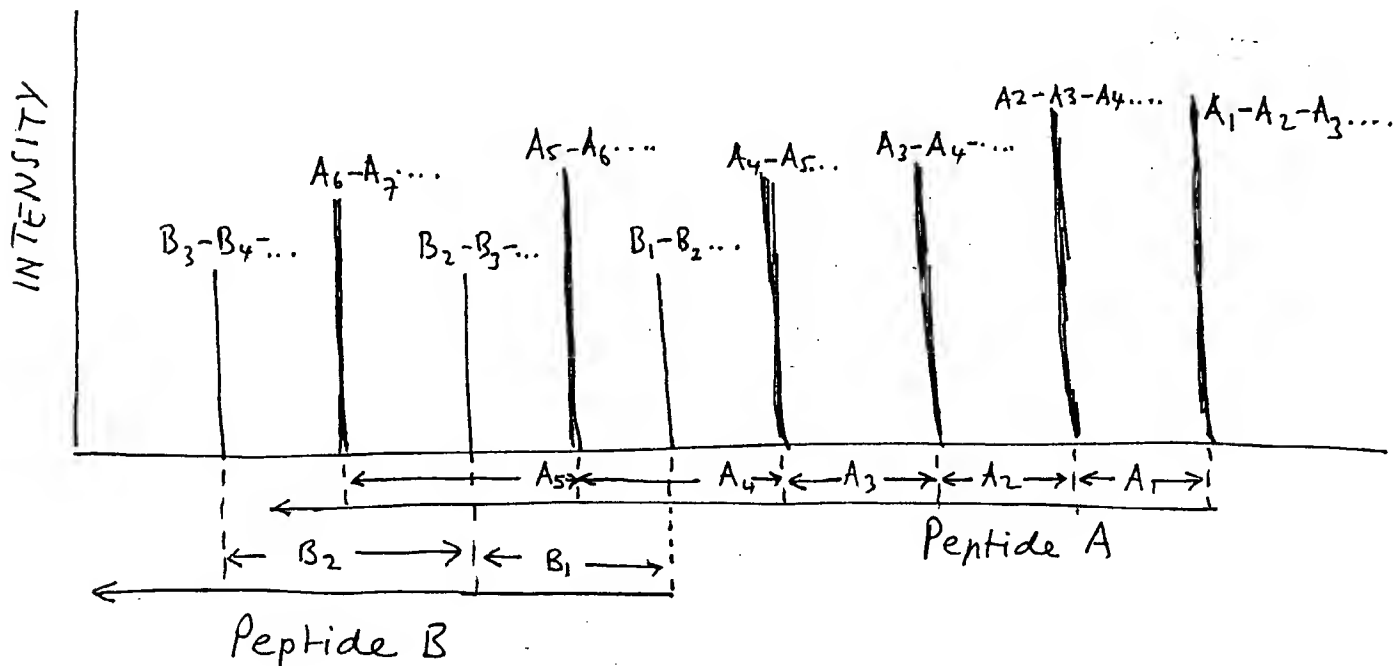
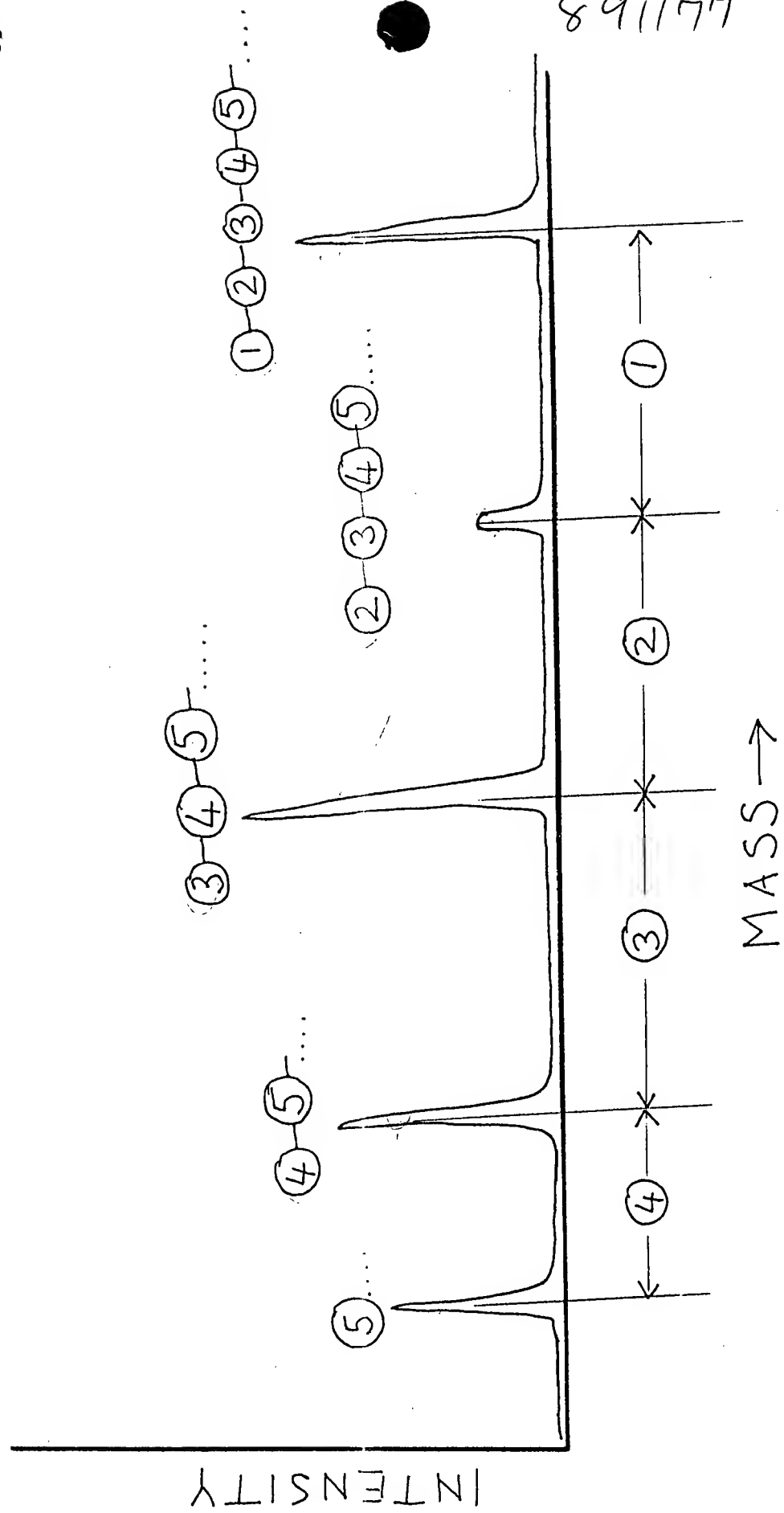
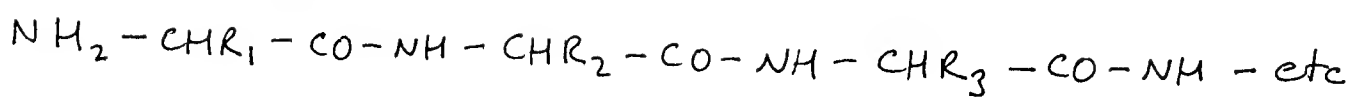


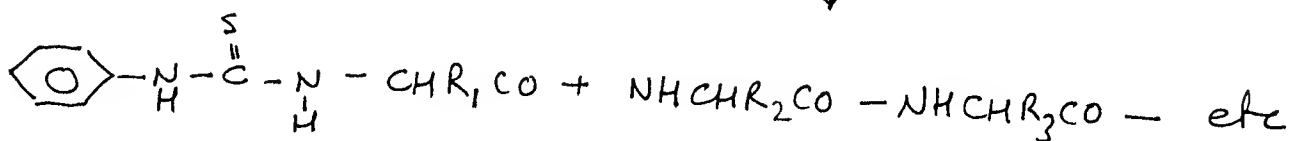
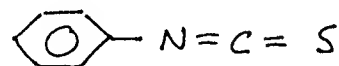
Figure 2

891177 6



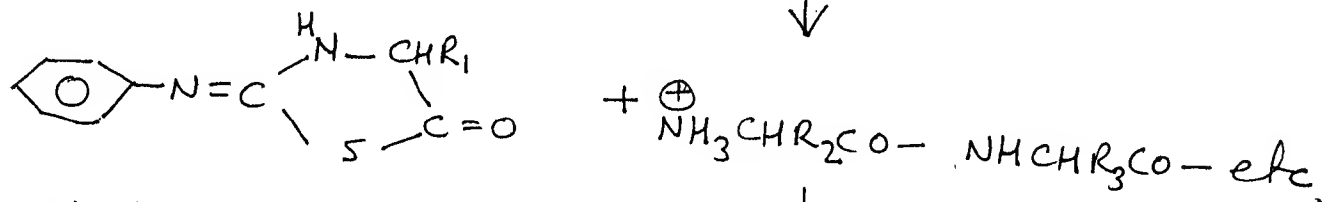


- ① Coupling: PITC in the presence of base.



- ② Wash, dry.

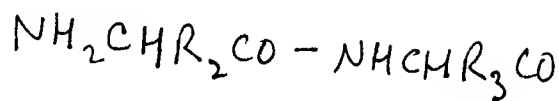
- ③ Cleavage: anhydrous acid



- ④ Wash (removes ATZ/PTH derivative)

- ⑤ Neutralize: base

- ⑥ Wash



Repeat steps 1 — 6

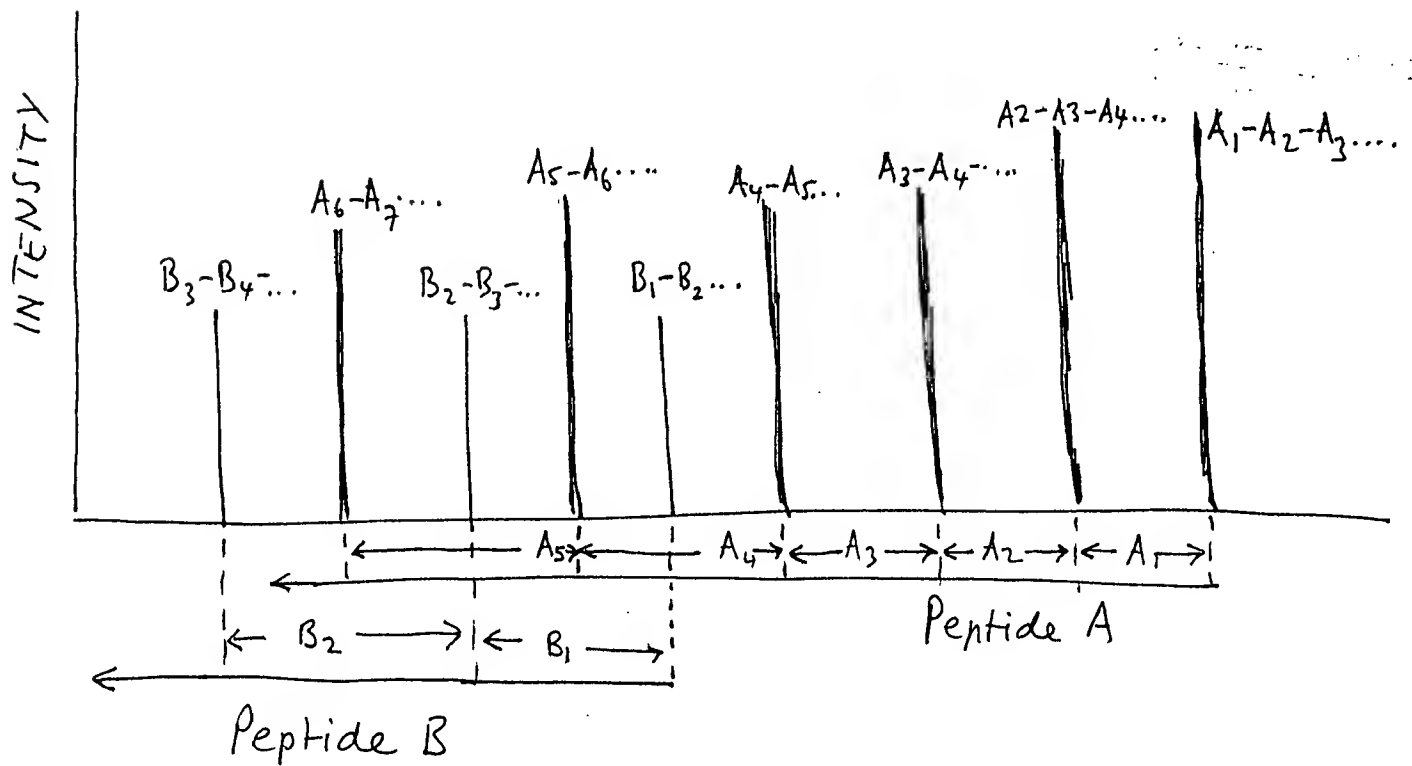
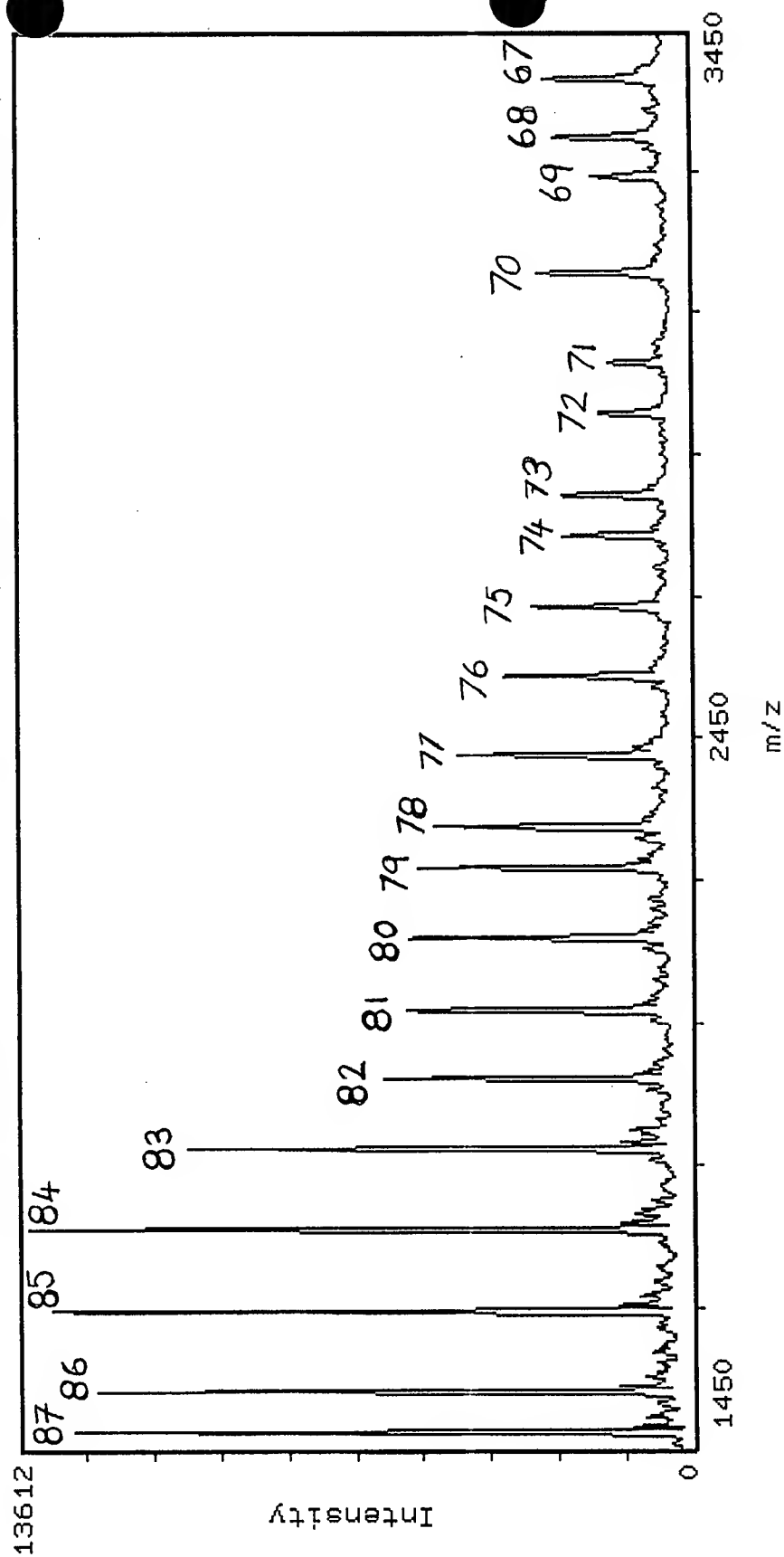


Figure A

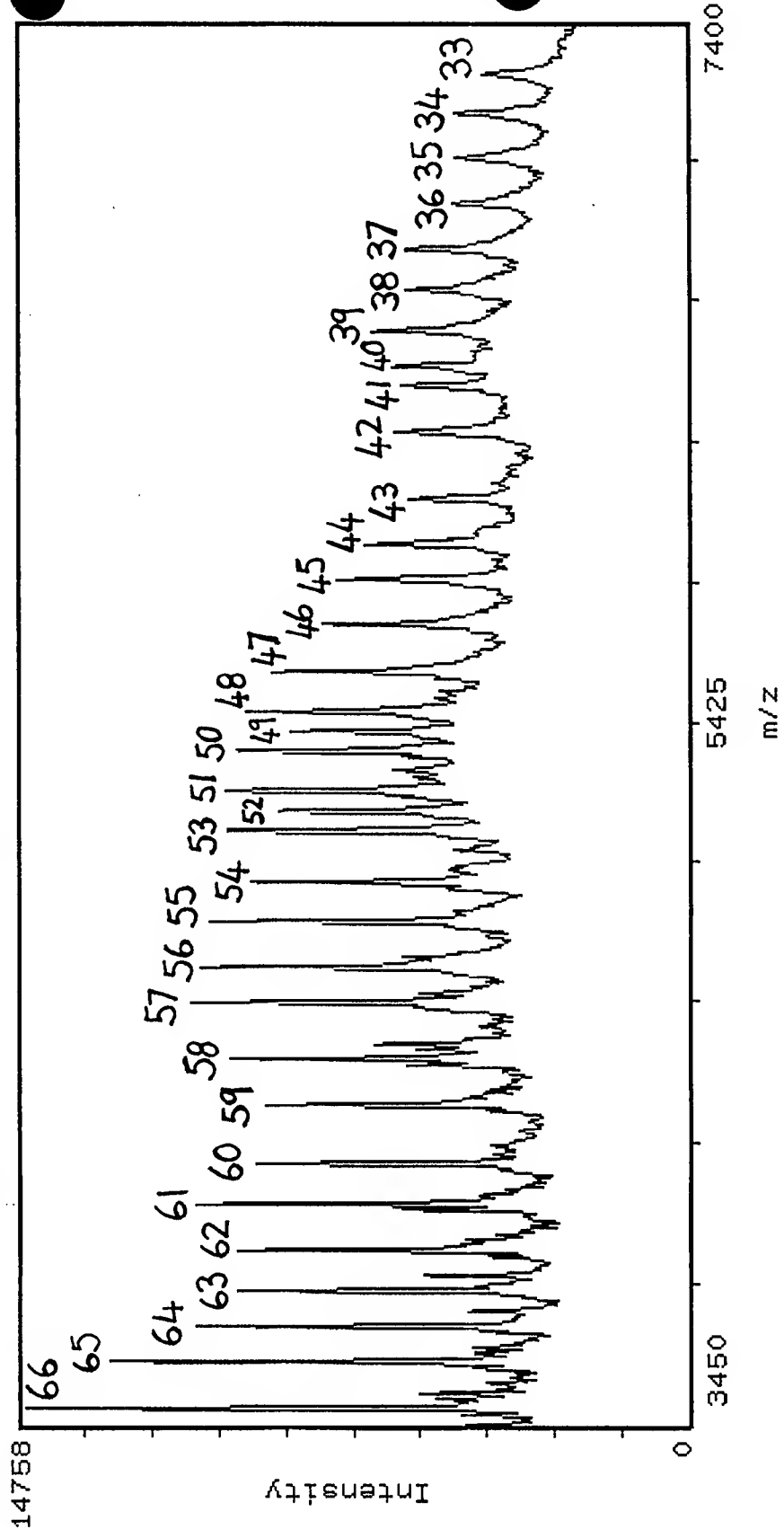
HIV-1 PROTEASE PEPTIDE LADDER (99-N, WHERE N=99,67)



891177

Figure B

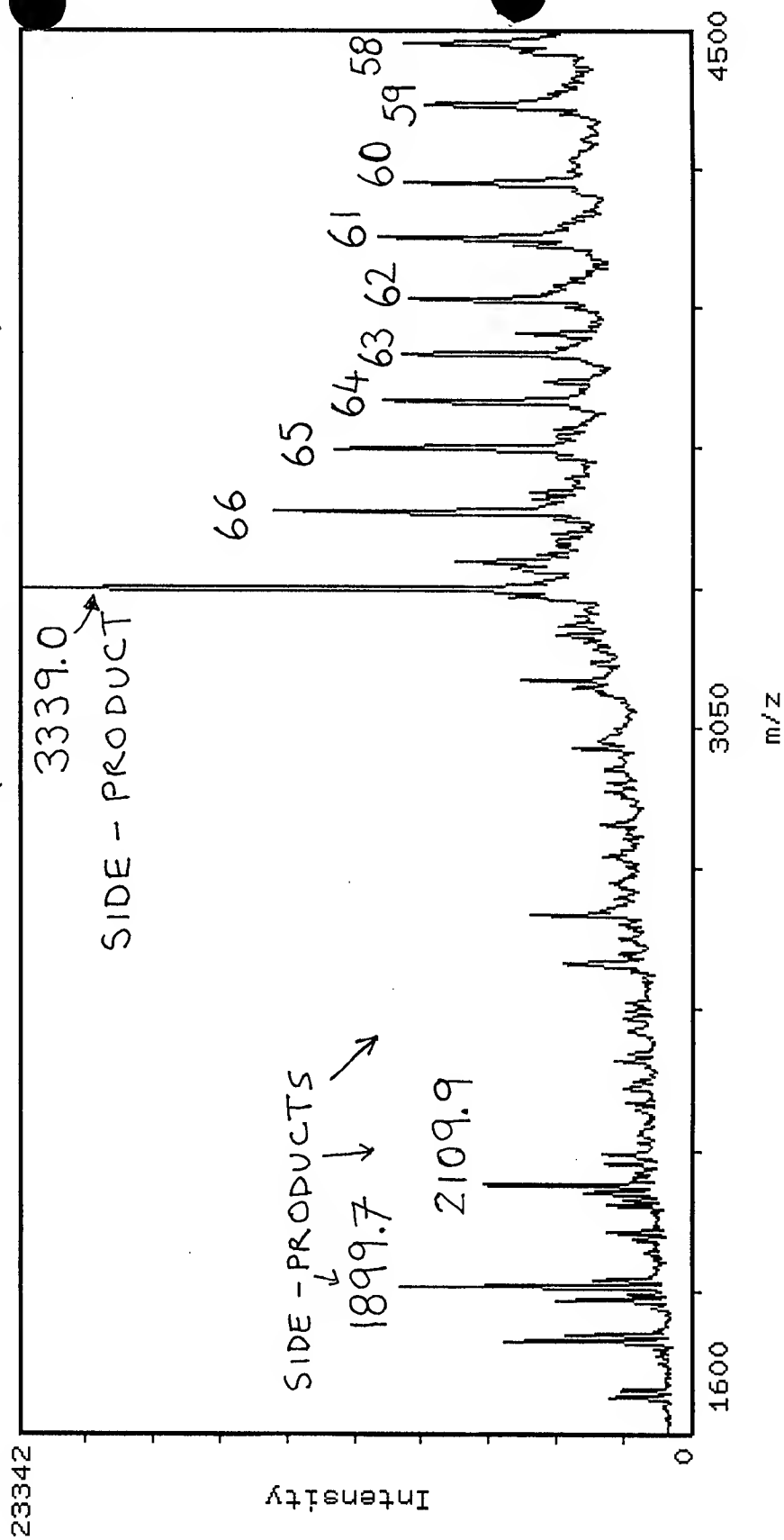
HIV-1 PROTEASE PEPTIDE LADDER (99-N, WHERE N=66,33)



891177

FIGURE C

LOW MASS REGION OF HIV-1 PROTEASE
PEPTIDE LADDER (99-N, WHERE N=66,33)



891177